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14. ABSTRACT
Vibrio harveyi is a Gram-negative bacterium found in tropical and temperate marine environments as a free-living organism or in association with aquatic animals. We report the first sequenced genome of a Vibrio harveyi strain, CAIM 1792, the etiologic agent of the ?bright red? syndrome of the Pacific white shrimp Litopenaeus vannamei.

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Draft Genome Sequence of the Shrimp Pathogen Vibrio harveyi CAIM 1792

Iliana Espinoza-Valles, Sonia Soto-Rodríguez, Robert A. Edwards, Zheng Wang, Gary J. Vora and Bruno Gómez-Gil

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GENOME ANNOUNCEMENT

Draft Genome Sequence of the Shrimp Pathogen *Vibrio harveyi* CAIM 1792

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***Vibrio harveyi* is a Gram-negative bacterium found in tropical and temperate marine environments as a free-living organism or in association with aquatic animals. We report the first sequenced genome of a *Vibrio* harveyi strain, CAIM 1792, the etiologic agent of the "bright red" syndrome of the Pacific white shrimp *Litopenaeus vannamei*.**

Vibrio harveyi is a member of the *Vibrio* core group and an organism with an important role in the study of bacterial autoinduction (6) and bioluminescence (3). It is also an important pathogen of marine fish and invertebrates (1), especially for shrimp (5). Strain CAIM 1792 has caused recurrent outbreaks of vibriosis known as "bright red" syndrome in *Litopenaeus vannamei* shrimp farms in northwestern Mexico since 2005 (7). While it is accepted that genome sequence information can greatly enhance our understanding of the molecular pathogenicity mechanisms responsible for *V. harveyi*, the recent discovery of the misidentification of the two purported *V. harveyi* strains for which the genomes were sequenced demonstrated that there is a lack of a representative *V. harveyi* genome (4).

Strain CAIM 1792 was sequenced using a 454 GS-FLX pyrosequencing approach (Life Sciences/Roche, Branford, CT). The high-throughput sequencing resulted in ~18-fold coverage (104,105,476 bases sequenced), and the 529,955 reads were assembled using the Newbler software (version 2.5.3) into 87 contigs. A genome-scale assembly was constructed with Mauve Genome Alignment software (version 2.3.1; Genome Evolution Laboratory, University of Wisconsin—Madison [http://asap.ahabs.wisc.edu]). The ordering of the contigs was tested by using the Scaffolding builder program (G. G. Z. Silva, B. E. Dutilh, D. Matthews, K. Elkins, A. M. Segall, R. A. Edwards, and E. A. Dinsdale, submitted for publication) and with the completed *Vibrio campbellii* ATCC BAA-1116 genome as a reference. BlastX queries were performed to validate assemblies containing coding sequences (CDS). The draft genome described in this study contains 21 gaps that are in the process of closure via PCR amplicon sequencing.

The assembled genome of CAIM 1792 is 5.84 Mbp in size with 5,328 RAST server-annotated CDS (2), and it has two chromosomes and a plasmid. The 3.50-Mbp chromosome I (Chr I) is composed of seven supercontigs and four contigs with 11 gaps and contains eight rRNA operons and at least 47 tRNAs. In comparison, the 2.24-Mbp chromosome II (Chr II) is composed of four supercontigs with seven gaps and contains one rRNA operon and at least 12 tRNAs. Similar to most sequenced *Vibrio* spp. strains, *V. harveyi* CAIM 1792 has a superintegron located in Chr I that is 87.2 Kbp in size and contains ~130 gene cassettes, of which 97 encode hypothetical proteins. The genome sequence also revealed >100 genes that encode putative virulence factors (e.g., hemolysins, proteases, chitinases, collagenases, iron acquisition, type I, II, III, IV, and VI secretion systems, RTX toxins, and vibriolysin) that, when combined with additional comparative genomic analyses with sequenced sister species such as *V. campbellii*, *V. parahaemolyticus*, *V. rotiferianus*, and *V. owensii*, will aid in revealing the underlying genetic assemblages responsible for pathogenicity, host range, environmental adaptation, and evolution within *V. harveyi* and the *Vibrio* core group.

Nucleotide sequence accession numbers. *Vibrio harveyi* CAIM 1792 has been deposited in the Collection of Aquatic Important Microorganisms (CAIM; www.ciad.mx/caim), and the genome sequence has been deposited in the GenBank database under accession number AHHQ00000000. The version described in this study is the first version, AHHQ01000000.

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The opinions and assertions contained herein are those of the authors and are not to be construed as those of the U.S. Navy, military service at large, or U.S. Government.

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